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Different pattern of expression of cellular oncogenes in human non-small-cell lung cancer cell lines.

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Altered and deregulated cellular oncogenes were found in many human solid tumors. Except for a few types of tumors that consistently exhibited specific altered proto-oncogenes, the majority of tumors are associated with a number of transcriptionally activated cellular oncogenes. In the heterologous group of non-small-cell lung cancer (NSCLC), nothing about a specific pattern of proto-oncogene expression is known. Therefore, we investigated the expression of a panel of cellular oncogenes in NSCLC cell lines. DNA and RNA from 11 established NSCLC cell lines (4 adenocarcinoma cell lines, 3 squamous cell carcinoma cell lines, 3 large-cell carcinoma cell lines and 1 mesothelioma cell line) were isolated and analysed using the Southern, dot blot and Northern hybridization technique. c-myc RNA expression was found in all NSCLC cell line, L-myc expression only in 1 adenocarcinoma cell line, N-myc and c-myb expression in none of the 11 cell lines examined. No c-myc amplification could be detected in the DNAs. v-sis-related mRNA was observed in 5/11 cell lines without association to a specific NSCLC subtype. v-src-related mRNA, found in all tested cells, exhibited increased levels in 1 adenocarcinoma cell line (A-549) compared to the other cell lines. Binding sites for epidermal growth factor (EGF) had been described previously in NSCL, therefore we found erbB homologue transcripts coding for the EGF receptor in all NSCLC cell lines. Also, c-raf1-, N-ras-, Ki-ras-, and H-ras-related RNA expression was observed in all lines. We conclude that L-myc, N-myc, and c-myb expression does occur less frequently in NSCLC than in SCLC. Also amplification does not appear to be an important mechanism by which the c-myc proto-oncogene is activated in NSCLC. A specific

pattern of oncogene expression could not be detected in NSCLC cells; each cell line examined showed its own pattern. However, transcriptional activation of a proto-oncogene like erbB, ras, raf, src, and c-myc, which are all involved in the progression pathway of EGF, may be a common feature of NSCLC.

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